Community structure and spatial distribution of gamasid mites associated with small mammals in Yunnan, China

HUANG Li-Qin, GUO Xian-Guo*, WU Dian, WANG Qiao-Hua

(Institute of Pathogens and Vectors, Dali University, Dali, Yunnan 671000, China)

Abstract: Ectoparasitic gamasid mites associated with small mammals have long been suspected to be the vectors of some zoonoses such as hemorrhagic fever with renal syndrome (HFRS) and rickettsialpox. In this paper, the results of wild investigations of the gamasid mites associated with small mammals in 28 counties of Yunnan, China is reported. The characteristics of community and describe the spatial distribution of gamasid mites along an environmental gradient are analyzed by using species richness, Shannon diversity index. In addition, the similarity of 18 mite infracommunities was compared by using hierarchical clustering analysis (SPSS 16.0). A total of 14 544 individuals of small mammals belonging to five orders (Rodentia, Insectivora, Scandentia, Lagomorpha and Carnivora), 10 families, 35 genera and 67 species were trapped, from which 80 791 individuals of gamasid mites representing 10 families, 33 genera and 112 species were collected. The results indicated that the dominant host species were *Rattus tanezumi*, *Apodemus chevrieri*, and *Eothenomys miletus*, while dominant gamasid mite species were *Laelaps nuttalli*, *L. echidninus* and *L. guizhouensis*. The mite infracommunities associated with *A. chevrieri*, *N. confucianus* and *R. tanezumi* exhibited the highest species richness, while mite infracommunities on *Suncus murinus*, *Apodemus chevrieri* and *Crocidura attenuata* presented the highest diversity. The results of cluster analysis showed that the similarity of most mite communities in accordance with the taxonomic relationship and the habitat of their corresponding small mammal hosts. The mite communities are clustered into the same group when their hosts are similar in zoological taxonomy and habitat selection. The horizontal patterns of gamasid mite species richness along a latitudinal gradient showed two peaks, the highest richness was recorded at the latitude 25°N to 26°N, while the vertical patterns presented a single-peak curve along the elevation gradient, peaking at the elevation of 2 000 m to 2 500 m. The diversity spatial distribution patterns of gamasid mites and their small mammal hosts showed the similar trends of single-peak curves which gradually increased and then decreased with increasing of latitude and elevation, peaking at the latitude 26°N to 27°N and the elevation of 2 000 m to 2 500 m. The results suggest that the community structure of gamasid mites in Yunnan Province has high species richness and diversity. The spatial distribution patterns of gamasid mites in Yunnan Province may be the results of the edge effect between the Oriental and Palaearctic realms.

Key words: Gamasid mites; small mammals; community structure; spatial distribution; cluster analysis; Yunnan

1 INTRODUCTION

Gamasid mites are arthropods characterized by extremely high interspecific variation in their ecology and feeding modes. Some species are free-living including soil-dwelling and plant-dwelling while some others are ectoparasites or nidicolous predators (Korallo-Vinarskaya *et al.*, 2007). Ectoparasitic gamasid mites are important medical arthropods, they not only infest human and cause severe allergic reaction, but also may play an important role in transmitting some zoonoses such as rickettsialpox and hemorrhagic fever with renal syndrome (HFRS), *etc.* (Baker *et al.*, 1956; Younis *et al.*, 1995). Yunnan Province is a focus area of HFRS, which has long been regarded as "the kingdom of animals and plants" of China. Although many studies have described the ecology of gamasid mites ranging from host-specificity to fauna in Yunnan Province (Guo, 1998, 1999a, 1999b; Men *et al.*, 2007; Luo *et al.*, 2007a), few studies have been conducted on the community structure and spatial distribution of the

gamasid mites in Yunnan Province, China (Guo, 1997; Guo and Qian, 2001). In this report, we analyze the community structure and species composition at the component and infracommunity levels, and present an analysis of spatial distribution of gamasid mites associated with small mammals from the horizontal and vertical levels.

2　MATERIALS AND METHODS

2.1　Study area and sampling

From 1990 to 2008, the field investigation were conducted in 28 counties (towns) in Yunnan Province (21°8′ – 29°15′ North and 97°31′ – 106°11′ East), China. The 28 investigated counties are Baoshan, Yangbi, Jianchuan, Lijiang, Heqing, Xiangelila, Gongshan, Weishan, Nanjian, Puer, Ninger, Weixi, Lanping, Dali, Binchuan, Xiangyun, Wenshan, Qiubei, Mengzi, Yuanjiang, Fuyuan, Qiaojia, Suijiang, Yingjiang, Gengma, Maguan, Hekou and Menghai. The gamasid mites were collected from the host skin and pelage of trapped small mammals.

Small mammals were captured yearly from June to August in 28 different counties. Captures were realized with Golden Cat® traps. Most rodents were captured using snap-traps; shrews, moles, sciurids and lagomorphs were live-captured using live traps (10 cm × 11 cm × 24 cm) (Guixi Mousetrap Apparatus Factory, Guixi, Jiangxi, China). About 200 – 300 traps were placed per day in each trapping site. Each trapping at one location lasted three nights (one trap session). Total trapping effort involved 315 000 trap nights and 420 sessions (15 sessions per location on average). The traps were baited with corn or oil-fried peanut, set just before sunset and checked soon after dawn. Each trapped small mammal was placed in an individual cloth bag in the field and transported to the laboratory for the collection of ectoparasites. All trapped animals were examined and identified to species based on external morphology, measurements and visible characters of dentition (Huang *et al.*, 1995). Some of the dubious specimens were confirmed by postmortem examination of skull. Each small mammal was thoroughly examined for ectoparasites over a large, square and white tray. Ectoparasites were located with the naked eyes by combing the hosts' pelage with fine-tipped forceps and preserved in 70% ethanol. After the sample was processed, all instruments were dried with disposable paper towels to reduce the chance of contamination. In the laboratory, individual mites were then washed several times in clean water to eliminate the alcohol and mounted with Hoyer's medium on microscope slides. After clearing and drying, each mite specimen was finally identified to species under the microscope according to the identification keys and some

other taxonomic literatures (Deng *et al.*, 1993). All procedures were performed according to animal care and use protocols approved by the Intramural Institutional Animal Care and Use Committee of Dali University. Representative individuals of small mammal and gamasid mite voucher specimens were deposited in the specimen repository of Institute of Pathogens and Vectors, Dali University, China.

2.2　Data analysis

In this paper, all the gamasid mites on a certain species of small mammal host were defined as one gamasid mite community. The constituent ratio (C_r), prevalence (P, proportion of infested rat hosts) and mean abundance (MA, mean number of gamasid mites per host examined) were calculated for each gamasid mite population (Margolis *et al.*, 1982; Whitaker, 1988; Bush *et al.*, 1997). Species accounting for more than 10% of the constituent ratio in the community were determined as dominant species while 1% to 10% common species and below 1% rare species (Xu *et al.*, 1999; Liu *et al.*, 2008). For each gamasid mite infracommunity, species richness (S = number of species represented), Simpson's dominant index [$D = \sum (P_i)^2$], Shannon diversity index [$H = - \sum (P_i \ln P_i)$] (Magurran, 1988), and Pielou evenness, [$E = H / \ln(S)$] were used to describe the infracommunity structure, where P_i = proportional abundance of a given species. $P_i = n_i / N$, n_i = the number of ith species and N = the total numbers of individuals of all species in the community (Simpson, 1949). To interpret the value of these indices, a higher number indicates a more diverse community. Based on hierarchical clustering analysis, the similarity of 18 mite infracommunities were compared by using Ward Method with squared Euclidian distance.

To discuss the geographical distribution trends of gamasid mites and their small mammal hosts with geographical gradient (longitudes, latitudes and altitudes), the investigated 28 counties were divided into five groups along a longitudinal, latitudinal and elevation gradient, respectively. Spatial distribution was analyzed at horizontal and vertical levels by using species richness, mean abundance and Shannon diversity index. Spearman rank correlation coefficient was used to describe the relationship of diversity index, mean abundance changing with the geographical gradient.

All analyses were carried out with SPSS 16.0 for Windows (SPSS Inc., Chicago, IL, 2006).

3　RESULTS

3.1　Component community

A total of 14 544 individuals of small mammals

were captured and identified as 10 families, 35 genera and 67 species in five orders (Rodentia, Insectivora, Scandentia, Lagomorpha and Carnivora). From the body surface of captured small mammal hosts, 80 791 individuals of gamasid mites representing 10 families, 33 genera and 112 species were collected. A list of the main 18 host species and 15 species of gamasid mites was presented in Table 1 and Table 2, respectively. The 15 mite species and 18 small mammal species presented the high constituent ratio values of 91.71% and 93.13%, respectively. Based on the constituent ratio of hosts and gamasid mites, *Rattus tanezumi* (26.53%), *Apodemus chevrieri* (12.86%), and *Eothenomys miletus* (12.39%) which account for 51.78% of the total, were determined as the dominant host species, while the dominant gamasid mite species were *Laelaps nuttalli* Hirst, 1915 (25.06%), *L.*

echidninus Berlese, 1887 (19.61%) and *L. guizhouensis* Gu *et* Wang, 1981 (12.93%), accounting for 57.60% of the total. Most small mammal host species have a variety of species (from 12 to 50 species) of gamasid mites on their body surface, and most mite species can parasitize on a very wide range of hosts (from 6 to 31 species). *Apodemus chevrieri* had the highest number of mite species, while *R. tanezumi*, *Mus pahari* and *R. nitidus* harbour the largest number of mite individuals (Table 1). On the other hand, *L. nuttalli* and *L. echidninus* tend to select a wide range of hosts and infest a large number of host individuals; on the contrary, the host range of *L. algericus* and *L. xingyiensis* are relatively narrow (Table 2). The results imply that the community structure of gamasid mites and their corresponding small mammal hosts in Yunnan is very complex.

Table 1 The number of individuals, constituent ratios (C_r) of and the number of species and individuals of mites on the 18 main species of small mammal host in Yunnan, China

Small mammal hosts	Number of host individuals	$C_r(\%)$	Number of mite species	Number of mite individuals
Rattus tanezumi	3 859	26.53	43	18 459
Apodemus chevrieri	1 870	12.86	50	3 018
Eothenomys miletus	1 802	12.39	41	2 258
Rattus norvegicus	1 262	8.68	31	6 102
Mus pahari	697	4.79	34	13 559
Rattus nitidus	580	3.99	32	11 765
Apodemus draco	540	3.71	26	562
Niviventer confucianus	464	3.19	44	5 394
Mus caroli	376	2.59	33	2 258
Apodemus sylvaticus	280	1.93	20	501
Apodemus latronum	278	1.91	18	204
Suncus murinus	254	1.75	25	196
Rattus rattus slandeni	253	1.74	37	842
Tupaia belangeri	237	1.63	19	159
Crocidura attenuata	235	1.62	22	139
Mus musculus	210	1.44	12	156
Niviventer fulvescens	197	1.35	29	7 058
Anourosorex squamipeis	151	1.04	24	2 445

Table 2 The number of individuals, constituent ratios (C_r) and the number of species and individuals of the parasitized hosts of the main 15 species of gamasid mites

Gamasid mites	Number of mite individuals	$C_r(\%)$	Number of host species	Number of host individuals
Laelaps nuttalli	20 248	25.06	28	1 518
Laelps echidninus	15 840	19.61	23	2 002
Laelaps guizhouensis	10 444	12.93	17	614
Laelaps turkestanicus	6 429	7.96	31	510
Laelaps traubi	4 165	5.16	25	397
Ornithonyssus bacoti	3 340	4.13	15	477
Laelaps chini	2 734	2.92	28	667
Dipolaelaps anourosorecis	2 358	2.45	15	86
Laelaps paucisetosa	1 979	2.39	9	364
Laelaps algericus	1 933	3.38	6	210
Hirstionyssus sunci	1 099	1.36	27	394
Laelaps xingyiensis	955	1.18	8	326
Laelaps fukienensis	923	1.14	11	46
Eulaelaps dremomydis	832	1.03	13	71
Eulaelaps shanghaiensis	815	1.01	9	101

3.2 Infracommunities

In this paper, we defined all the gamasid mites from one species of hosts as a gamasid mite infracommunity, and then there were 18 mite infracommunities for study. We found that the small mammal hosts *Niviventer fulvescens*, *Mus pahari* and *Niviventer confucianus* presented the highest prevalence (86.29%, 85.65% and 81.03%, respectively). In addition, the infracommunities of *Niviventer fulvescens* (35.83), *Rattus nitidus* (20.28) and *Mus pahari* (19.49) presented the highest mean abundance, which means that these host species usually have a large number of mites on their body surface. Of the 18 gamasid mite infracommunities, the mite infracommunities associated with *Apodemus chevrieri*,

Niviventer confucianus and *Rattus tanezumi* exhibited the highest species richness (50, 44 and 43 species), while mite infracommunities on *Suncus murinus*, *Apodemus chevrieri* and *Crocidura attenuata* presented the highest Shannon diversity (1.184, 1.170 and 1.107) and evenness (0.841, 0.689 and 0.824), but the lowest Simpson's dominance indices (0.095, 0.110 and 0.108) respectively (Table 3). The lower diversity was recorded in the mite infracommunities on *M. pahari*, *M. caroli* and *Anowrosorex squamipes*, which was because certain mites dominated the majority of the infracommunities. The results show that the community structure of gamasid mites in Yunnan has high species richness and diversity.

Table 3 Comparison of species richness (S), prevalence (P), mean abundance (MA), Simpson's index (D), Shannon diversity index (H) and evenness (E) of 18 gamasid mite infracommunities

Infracommunities	S	P (%)	MA	D	H	E
Suncus murinus	25	30.31	0.77	0.095	1.184	0.841
Apodemus chevrieri	50	32.51	1.66	0.110	1.170	0.689
Crocidura attenuata	22	17.87	0.59	0.108	1.107	0.824
Apodemus draco	26	45.56	1.04	0.191	0.965	0.682
Apodemus sylvaticus	20	36.43	1.79	0.148	0.961	0.739
Rattus rattus slandeni	37	46.64	3.38	0.179	0.942	0.601
Tupaia belangeri	19	18.99	0.67	0.183	0.941	0.736
Apodemus latronum	18	26.62	0.73	0.160	0.921	0.733
Eothenomys miletus	41	41.45	1.25	0.474	0.666	0.413
Niviventer confucianus	44	81.03	11.63	0.312	0.629	0.383
Rattus norvegicus	31	32.09	4.84	0.304	0.613	0.411
Niviventer fulvescens	29	86.29	35.83	0.309	0.582	0.398
Mus musculus	12	11.9	0.74	0.466	0.527	0.489
Rattus tanezumi	43	48.07	4.78	0.421	0.523	0.320
Rattus nitidus	32	62.59	20.28	0.440	0.446	0.296
Mus pahari	34	85.65	19.49	0.592	0.391	0.255
Mus caroli	33	64.36	6.01	0.698	0.356	0.235
Anowrosorex squamipes	24	52.32	16.19	0.843	0.205	0.149

Although most of the gamasid mite species can parasitize on many species of hosts, but they have relatively fixed principal host species (Table 4), for example, *Laelaps algericus* achieves the maximum abundance (1 877/1 933) on *M. caroli*, while *Dipolaelaps anourosorecis* (2 243/2 358) mainly parasitize on the host *Anowrosorex squamipes*, *Laelaps chini* mainly parasitize on the genus *Eothenomys*; but *Laelaps nuttalli* and *Laelps echidninus* tend to select a relatively wide realm of hosts. More interesting, a large number of the mites *L. paucisetosa* (1 949/1 979), *L. guizhouensis* (10 227/10 444) and *L. xingyiensis*

(914/955) were found on the host *M. pahari*, they seemed to prefer on the same host.

3.3 Clustering analysis

Based on the composition of 15 dominant mite species and the characteristic of 18 gamasid mite infracommunities, squared Euclidian distance was chosen to measure the similarities between every two infracommunities. Ward Method in hierarchical clustering analysis was used to compare the 18 gamasid mite infracommunities. The hierarchical clustering result was presented as a dendrogram (Fig. 1). The result showed that the mite infracommunities tend to

Table 4 Number of individuals of 15 species of gamasid mites parasitized on 18 main species of small mammal hosts

Host species	Number of mite individuals														
	Laelaps nuttalli	*Laelaps echidninus*	*Laelaps guizhouensis*	*Laelaps turkestanicus*	*Laelaps traubi*	*Ornithonyssus bacoti*	*Laelaps chini*	*Dipolaelaps anourosorecis*	*Laelaps paucisetosa*	*Laelaps algericus*	*Hirstionyssus sunci*	*Laelaps xingyiensis*	*Laelaps fukienensis*	*Eulaelaps dremomydis*	*Eulaelaps shanghaiensis*
Rattus tanezumi	10 697	5 188	4	69	86	1 394	3	0	0	2	131	1	0	0	0
Apodemus chevrieri	152	313	49	147	56	5	61	9	6	0	369	1	0	0	752
Eothenomys miletus	7	61	5	15	37	1	1 540	0	3	0	23	0	3	4	20
Rattus norvegicus	2 446	1 634	5	13	5	1 627	20	0	2	9	126	4	0	0	2
Mus pahari	0	22	10 227	38	0	0	36	2	1 949	21	62	914	2	0	0
Rattus nitidus	5 795	5 217	13	7	8	136	8	0	5	0	140	0	35	0	0
Apodemus draco	9	1	0	28	40	10	36	0	0	0	2	0	0	0	3
Niviventer confucianus	35	1181	11	2 426	1 334	3	12	1	0	0	13	1	218	2	1
Mus caroli	180	6	27	32	0	1	2	0	7	1 877	4	21	0	0	0
Apodemus sylvaticus	121	44	50	31	2	0	0	5	0	0	6	0	0	0	0
Apodemus latronum	28	1	0	0	2	0	5	0	1	0	20	0	0	1	10
Suncus murinus	46	9	1	2	0	13	3	9	0	0	10	0	0	0	0
Rattus rattus slandeni	241	185	4	166	8	14	1	1	0	0	94	0	0	0	2
Tupaia belangeri	2	4	0	5	24	8	1	0	0	0	11	0	0	5	0
Crocidura attenuata	29	16	2	5	0	10	3	4	0	0	12	0	0	0	0
Mus musculus	10	10	2	1	0	103	0	0	1	23	0	0	0	0	0
Niviventer fulvescens	17	1 369	0	3 054	1 971	0	0	0	1	0	4	1	561	0	0
Anowrosorex squamipes	32	51	0	1	0	0	14	2 243	0	0	43	0	0	0	0

cluster into the same group when their corresponding small mammal hosts belong to the same group in zoological taxonomy. For example, the small mammal hosts, *A. latronum*, *A. sylvaticus* and *A. draco* belong to the same family in zoological taxonomy, and the mite infracommunities on those hosts were merged into the same group. The similar clustering results also happened in the mite infracommunities on *R. tanezumi*, *R. nitidus* and *R. norvegicus* which belong to the same genus (*Rattus*) in the same family (Muridae), and the mite infracommunities on *M. pahari* and *M. caroli* which belong to same genus (*Mus*) in the same family (Muridae). The small mammal hosts, *A. latronum*, *A. sylvaticus* and *A.*

draco, belong to the same genus (*Apodemus*) in the same family in the taxonomy, and the mite infracommunities on those hosts were merged into the same group, too. Some of the mite infracommunities, however, were exceptions. The mite infracommunity on *Mus musculus* was far from those on *M. pahari* and *M. caroli* though their corresponding hosts were in the same family. The difference in habitat selection of the hosts may be the suitable explanation: because *M. musculus* are house mice that mostly inhabit indoor environments, while *M. pahari* and *M. caroli* are field mice which mainly distribute in outdoor cultivated habitats (fields, dry lands and bush areas).
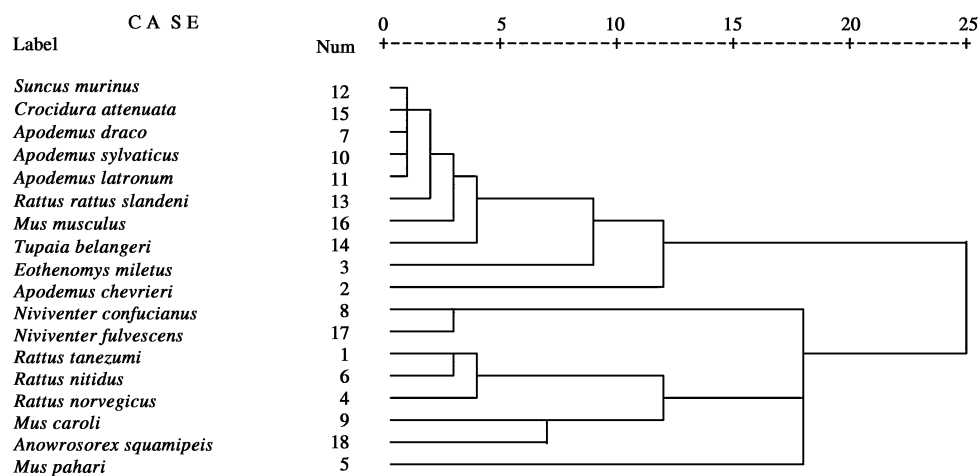
Fig. 1 Hierarchical clustering dendrogram of 18 gamasid mite infracommunities in Yunnan, China

3.4 Spatial distribution

3.4.1 Species richness and mean abundance patterns of gamasid mites : The horizontal patterns of gamasid mite species richness along a latitudinal gradient showed two peaks, the highest species richness was recorded at 25° to 26°N where 82 species of mites were found. The mean abundance of mites presented about a decreased trend along the latitudinal gradient ($r_s = -0.900$, $P = 0.037$) (Fig. 2). The vertical patterns of mites were quite different from that of the horizontal patterns along a latitudinal gradient. We found that the species richness and mean abundance of gamasid mites both gradually increased and then decreased as a single-peak curve with the increase of elevation, The richness peaked at the elevation of 2 000 m to 2 500 m where 73 species of mites were found, while mean abundance peak appeared in the areas from 1 500 to 2 000 m above sea level (Fig. 3).

The spatial distribution of the density of 15 dominant gamasid mites was shown in Fig. 5 and Fig. 6. The number 1 to 15 on the *x*-axis stand for *L. nuttall*, *L. echidninus*, *L. guizhouensis*, *L. turkestanicus*, *L. traubi*, *O. bacoti*, *L. chini*, *D. anourosorecis*, *L. paucisetosa*, *L. algericus*, *H. sunci*,

L. xingyiensis, *L. fukienensis*, *E. dremomydis*, *E. shanghaiensis*, respectively. At the horizontal levels, *L. nuttalli*, *L. echidninus*, *L. turkestanicus*, *L. traubi* were widely distributed species at the five latitudes. At the vertical levels, *L. nuttalli*, *L. echidninus*, *L. turkestanicus*, and *O. bacoti* were widely distributed at the five altitudes. The results indicated that *L. nuttalli*, *L. echidninus* and *L. turkestanicus* were widely distributive species in Yunnan Province.
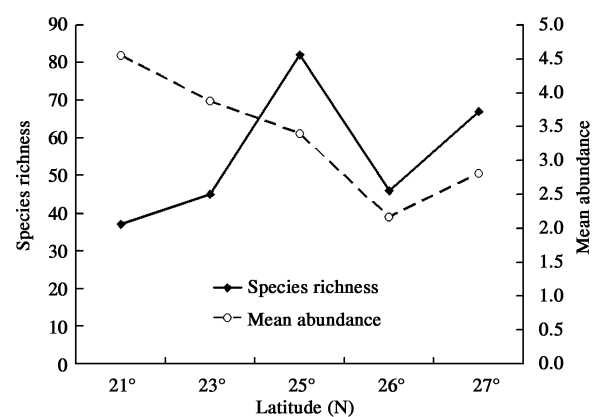

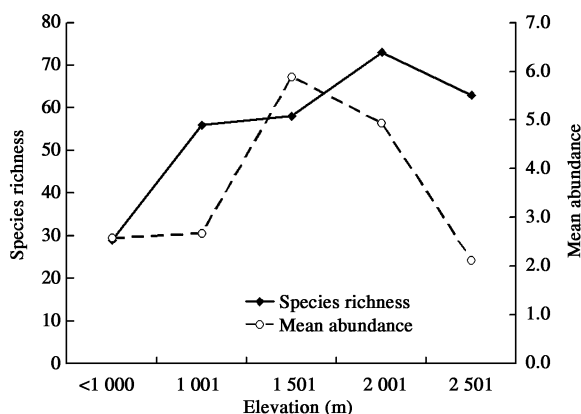Fig. 2 Horizontal distribution of gamasid mite richness and mean abundance

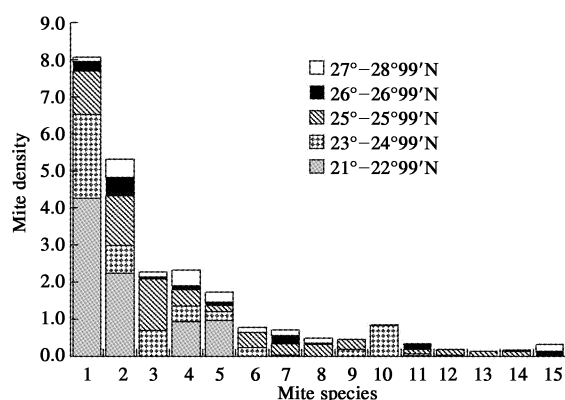Fig. 3 Vertical distribution of gamasid mite richness and mean abundance

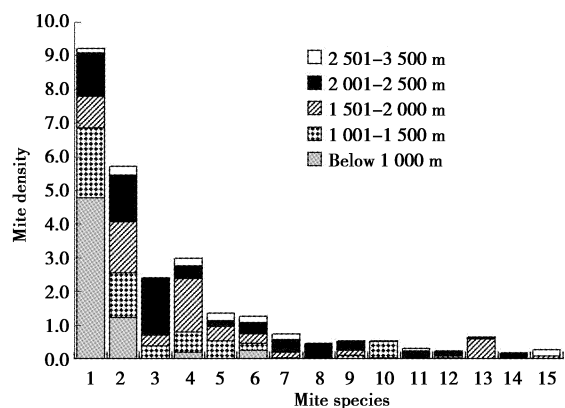Fig. 4 Density of 15 main gamasid mites at different latitudes

Fig. 5 Density of 15 main gamasid mites at different altitudes

3.4.2 Diversity patterns of mites and small mammal hosts: Figs. 7, 8, 9 showed the diversity patterns of small mammal hosts and gamasid mites along a longitudinal, latitudinal and altitudinal gradient, respectively. Our findings suggested that with increasing of longitude, the diversity of mites and their hosts decreased gradually from the west to the east (for mites, $r_s = -1.000$, $P < 0.01$; for hosts, $r_s = -0.900$, $P = 0.037$) (Fig. 6). With increasing of latitude, both diversity of small mammals and gamasid mites showed the similar trend of increased first and then decreased (single-peak curve patterns) from the

south to the north, peaking at 26° to 27°N (Fig. 7). The vertical patterns of mites and small mammal hosts along the altitudinal gradient were similar to the horizontal pattern, peaking at the elevation of 2 000 to 2 500 m (Fig. 8).
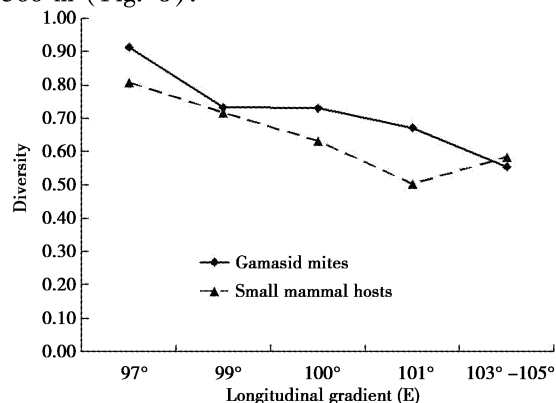

Fig. 6 Diversity patterns of gamasid mites and their small mammal hosts along a longitudinal gradient
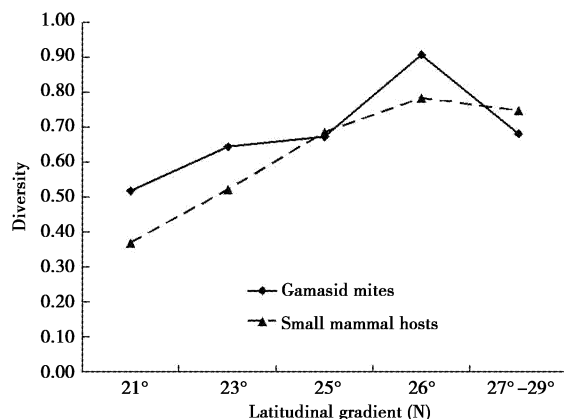

Fig. 7 Diversity patterns of gamasid mites and their small mammal hosts along a latitudinal gradient
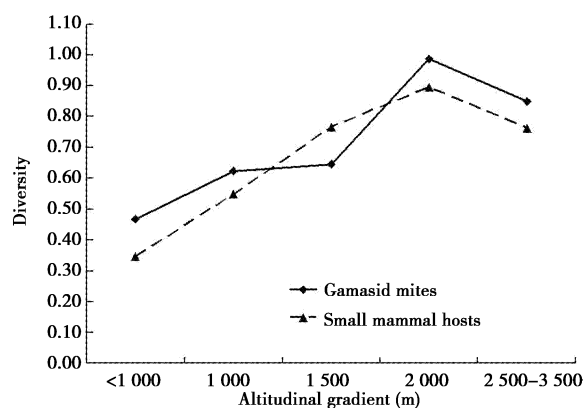

Fig. 8 Diversity patterns of gamasid mites and their small mammal hosts along an altitudinal gradient

4 DISCUSSION

Parasite community structure is usually measured by diversity indices which provide more information about community composition than simply species

richness. The diversity of gamasid mite communities in Yunnan Province was different from host species to species. The complicated community structures of gamasid mites were closely related to the diversity of small mammal hosts and the landscape. Increase in the diversity of the host community decreased the prevalence of mite infection in its main host, which can be viewed as a "dilution effect" phenomenon (Krasnov et al., 2007).

Host-specificity and host-selection may have important ecological and evolutionary implications (Radovsky, 1985; Krasnov et al., 2004). A high degree of host-specificity can be viewed to have high coevolution with their hosts, and vice versa. From the uneven distribution of gamasid mite species among different host species, we found that some mite species usually parasitized relatively on one or two species of dominant hosts, such as L. paucisetosa, L. xingyiensis and Dipolaelaps anourosorecis, while some other species tended to select a very wide realm of hosts, such as L. nuttalli and L. echidninus. On one hand, low host specificity may limit the risk of extinction and provide more immediate fitness benefits to parasites, such that selection may favour evolution toward a generalist strategy (Poulin et al., 2006). But from the point of epidemiology, low host-specific mites may be more likely to increase the chance of disease transmission in different species of hosts (Guo, 1998). According to the reports of epidemiology surveillance in Yunnan Province, R. tanezumi and R. norvegicus are the main hosts that carrying HFRS virus, on which L. nuttalli and L. echidninus achieve the maximum abundance (Yang et al., 2006).

In this paper, the gamasid mite communities were divided into different clustering groups based on their species composition and community structures. The results indicate that gamasid mite communities are not only related to the hosts' taxonomy status but also possibly influenced by the hosts' habitat. When the habitat selection of the hosts is similar, the closer the taxonomic position of the corresponding hosts is, the more similar the mite communities on their body will be. Our results are consistent with the idea that host biology may be a key determinant of the structure of parasite communities (González and Poulin 2005; Luo et al., 2007b). The abundance of the hosts and the species composition of host communities are crucial factors affecting the distribution and abundance of parasites (Anderson and May, 1978; Arneberg et al., 1997).

Biodiversity change along the environmental gradient is one of the focal points in the research of biodiversity. In this paper, we analyzed the mite species richness and diversity patterns of gamasid mites and their small mammal hosts from the horizontal and vertical distribution. For the horizontal distribution, the results demonstrated a geographical distribution trend that diversity of gamasid mites decreased gradually from the west to the east, first increased and then decreased from the south to the north. The mean abundance of gamasid mites decreased with the latitude increasing. This was in line with the former study of Wallace (1878), which indicated that species density decreases with the increase of latitudes. For the vertical distribution, previous studies indicate that species diversity along the altitudinal gradient has two main distribution patterns: species diversity decreases in general with the increase of altitude, the other is a single-peak curve pattern (which increases first and then decreases) with the altitude increasing. The vertical patterns present a single-peak curve along the elevation gradient. The horizontal patterns of species diversity were similar to the vertical pattern in our study. Our study demonstrated that the diversity of small mammal and gamasid mites both showed the single-peak curve patterns along the elevation gradient, peaking at the elevation of 2 000 to 2 500 m. The highest species richness was recorded at latitude 25° to 26°N while diversity peaking at 26° to 27°N, which may be the result of an edge effect between the Oriental and Palaearctic realms. The transitional zone of the two faunal realms ranged from 23° to 29°N and formed an overlap zone and divergence center at 25° to 27°N. The horizontal patterns of gamasid mite species richness along a latitudinal gradient showed two peaks, which revealed a transitional fluctuation of mite species in the overlap zone of the two realms. Because of the edge effect and complex landscape, both small mammals and gamasid mites showed high diversity, suggesting that this may be the core areas for diversity conservation, distribution and differentiation in China (Gong et al., 2007). In addition, either the horizontal or the vertical distribution patterns of gamasid mites are similar to that of their small mammal hosts, which may be another evidence of coevolution between gamasid mites and their corresponding small mammal hosts.

References

Anderson RM, May RM, 1978. Regulation and stability of host-parasite

population interactions. I. Regulatory processes. *Journal of Animal Ecology*, 47: 219 –247.

Arneberg P, Skorping A, Read AF, 1997. Is population density a species character? Comparative analyses of the nematode parasites of mammals. *Oikos*, 80: 289 –300.

Baker EW, Evans TM, Gould DJ, Hull WB, Keegan HL, 1956. A Manual of Parasitic Mites of Medical or Economic Importance. National Pest Control, Association Inc., New York. 170 pp.

Bush AO, Lafferty KD, Lotz JM, Shostak AW, 1997. Parasitology meets ecology on its own terms: Margolis *et al.* revisited. *Journal of Parasitology*, 83: 575 –583.

Deng GF, Wang DQ, Gu YM, Meng YC, 1993. Economic Insect Fauna of China. Fasc. 40. Acari: Dermanyssoidea. Science Press, Beijing. [邓国藩，王敦清，顾以铭，1993. 中国经济昆虫志，第 40 册，蜱螨亚纲，蜱刺螨总科. 北京：科学出版社]

Gong ZD, Zhang LY, Duan XD, Feng XG, Ge JQ, Li DM, Liu QY, 2007. Species richness and fauna of fleas along a latitudinal gradient in the Three Parallel Rivers landscape, China. *Biodiversity Science*, 15(1): 61 –69. [龚正达，张丽云，段兴德，冯锡光，葛军旗，栗冬梅，刘起勇，2007. 中国"三江并流"纵谷地蚤类丰富度与区系沿纬度梯度的水平分布格局. 生物多样性，15(1): 61 – 69]

González MT, Poulin R, 2005. Spatial and temporal predictability of the parasite community structure of a benthic marine fish along its distributional range. *International Journal for Parasitology*, 35: 1 369 –1 377.

Guo XG 1999b. Species-abundance distribution and expected species estimation of the gamasid mite community in western Yunnan, China. *Systematic and Applied Acarology*, 4: 49 –56.

Guo XG, 1997. Spatial pattern analysis of *Laelaps echidninus* and *Laelaps nuttalli* using Iwao's method and a significance test of random deviation. *Systematic and Applied Acarology*, 2: 89 –93.

Guo XG, 1998. Host-specificity and host-selection of gamasid mites (Acari: Gamasina). *Systematic and Applied Acarology*, 3: 29 –34.

Guo XG, 1999a. Cluster of ectoparasitic gamasid mites and their small mammal hosts in different habitat regions in western Yunnan. *Systematic and Applied Acarology*, 4: 39 –48.

Guo XG, Qian TJ, 2001. Sex ratio and age structure of gamasid mites from small mammals in western Yunnan, China. *Entomologia Sinica*, 8: 166 –174.

Huang WJ, Chen YX, Wen YX, 1995. Rodents of China. Fudan University Press, Shanghai. 308 pp. [黄文几，陈延熹，温业新，1995. 中国啮齿类. 上海：复旦大学出版社. 308 页]

Korallo-Vinarskaya NP, Krasnov BR, Vinarski MV, Shenbrot GI, Mouillot D, Poulin R, 2007. Stability in abundance and niche breadth of gamasid mites across environmental conditions, parasite identity and host pools. *Evolutionary Ecology*, 23: 329 –345.

Krasnov BR, Shenbrot GI, Khokhlova IS, Poulin R, 2004. Relationships between parasite abundance and the taxonomic distance among a parasite's host species: an example with fleas parasitic on small mammals. *International Journal for Parasitology*, 34: 1 289 –1 297.

Krasnov BR, Stanko M, Morand S, 2007. Host community structure and infestation by ixodid ticks: Repeatability, dilution effect and ecological specialization. *Oecologia*, 154: 185 –194.

Liu JY, Du H, Tian GB, Yu PH, Wang SW, Peng H, 2008. Community structure and diversity distributions of small mammals in different sample plots in the eastern part of Wuling Mountains. *Zoological Research*, 29: 637 –645.

Luo LP, Guo XG, Qian TJ, Wu D, Men XY, Dong WG, 2007a. Similarity of ectoparasitic gamasid mite (Acari: Parasitiformes: Mesostigmata) communities on small mammals in Yunnan, China. *Acta Zoologica Sinica*, 53: 208 –214. [罗礼溥，郭宪国，钱体军，吴滇，门兴元，董文鸽，2008. 中国云南小兽体表革螨的群落相似性. 动物学报，53: 208 –214]

Luo LP, Guo XG, Qian TJ, Wu D, Men XY, Dong WG, 2007b. Distribution of gamasid mites on small mammals in Yunnan Province, China. *Insect Science*, 14: 71 –78.

Magurran A, 1988. Ecological Diversity and Its Measurement. Croon Helm Limited, Australia. 179 pp.

Margolis L, Esch GW, Holmes JC, Kuris AM, Schad GA, 1982. The use of ecological terms in parasitology (report of an *ad hoc* committee of the American Society of Parasitologists). *Journal of Parasitology*, 68: 131 –133.

Men XY, Guo XG, Dong WG, Niu AQ, Qian TJ, Wu D, 2007. Ectoparasites of Chevrier's field mouse, *Apodemus chevrieri*, in a focus of plague in southwest China. *Medical and Veterinary Entomology*, 21: 297 –300.

Poulin R, Krasnov BR, Shenbrot GI, Mouillot D, Khokhlova IS, 2006. Evolution of host specificity in fleas: Is it directional and irreversible? *International Journal for Parasitology*, 36(2): 185 –191.

Radovsky FJ, 1985. Evolution of mammalian mesostigmatid mites. In: Kim KC ed. Coevolution of Parasitic Arthropods and Mammals. John Wiley, New York. 441 –504.

Simpson EH, 1949. Measure of diversity. *Nature*, 163: 668.

Wallace TR, 1878. Tropical Nature and Other Essays. Macmillian, London.

Whitaker JOJr, 1988. Collecting and preserving ectoparasites for ecological study. In: Kunz TH ed. Ecological and Behavioral Methods for the Study of Bats. Smithsonian Institution Press, Maryland, Washington DC. 459 –474 .

Xu ZH, Yang BL, Hu G, 1999. Formicidae ant communities in fragments of montane rain forest in Xishuangbanna, *China*. *Zoological Research*, 20(4): 288 –293. [徐正会，杨比伦，胡刚，1999. 西双版纳片断山地雨林蚁科昆虫群落研究. 动物学研究，20 (4): 288 –293]

Yang WH, Zhang HL, Mi ZQ, Zhang YZ, Zhang YZ, Ya HX, Feng Y, Yuan QH, 2006. Surveillance of hemorrhagic fever with renal syndrome in Yunnan Province, China, in 2004. *Chinese Journal of Vector Biology and Control*, 17(2): 112 –114. [杨卫红，张海林，米竹青，张云智，章域震，亚红祥，冯云，袁庆红，2006. 2004 年云南省肾综合征出血热监测研究. 中国媒介生物学及控制杂志，17(2): 112 –114]

Younis TA, Fayad ME, EI-Hariry MA, Morsy TA, 1995. Interaction between acari ectoparasites and rodents in Suez Governorate, Egypt. *Journal of the Egyptian Society of Parasitology*, 25: 377 –394.

中国云南小兽寄生革螨的群落结构和空间分布

黄丽琴，郭宪国*，吴　滇，王乔花

（大理学院病原与媒介生物研究所，云南大理，671000）

摘要：寄生在小兽体表的革螨可能是传播肾综合征出血热和立克次体痘等人兽共患病的媒介。本文报道了云南省28个县（市）小兽体表革螨的野外调查结果，运用物种数、平均丰富度和 Shannon 多样性指数对小兽寄生革螨的群落特征和沿环境梯度的空间分布进行了研究，并用系统聚类分析法（SPSS 16.0 软件）对18种主要小兽的革螨群落相似性进行了比较。在云南省28个县（市）共捕获到小兽 14 544 头，隶属于5目（啮齿目、食虫目、攀鼩目、兔形目、食肉目）10科35属67种，在捕获的小兽体表采集到革螨 80 791 头，经鉴定属于10科33属112种。结果分析表明：主要的宿主动物为黄胸鼠 *Rattus tanezumi*、齐氏姬鼠 *Apodemus chevrieri* 和大绒鼠 *Eothenomys miletus*；纳氏厉螨 *Laelaps nuttalli*、毒厉螨 *L. echidninus* 和贵州厉螨 *L. guizhouensis* 为革螨的优势种。齐氏姬鼠 *A. chevrieri*、社鼠 *N. confucianus* 和黄胸鼠 *R. tanezumi* 体表寄生的革螨种类最多；臭鼩鼱 *Suncus murinus*、齐氏姬鼠 *A. chevrieri* 和灰麝鼩 *Crocidura attenuata* 的革螨群落多样性最高。聚类分析结果表明，大部分革螨群落的相似程度与相应小兽的亲缘关系及所处生态环境的相似性是基本一致的，分类地位和生境选择相似的小兽，它们的革螨群落也被聚为一类。革螨物种数沿纬度梯度的水平分布呈现两个峰值，最大峰值出现在 25°～26°N 之间；沿海拔梯度的垂直分布呈单峰分布格局，峰值在海拔 2 000～2 500 m 之间。革螨和小兽的多样性沿纬度梯度和海拔梯度的空间分布趋势也均表现出随着纬度和海拔的升高而先升高后降低的单峰型分布格局，峰值分别出现在北纬 25°～27°N 和海拔 2 000～2 500 m 之间。结果提示云南革螨群落种类丰富，多样性高。云南革螨物种数和多样性的分布格局可能直接受到古北和东洋两区系边缘效应的影响。

关键词：革螨；小兽；群落结构；空间分布；聚类分析；云南

（责任编辑：袁德成）